



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 144542

**TO:** Anne Holleran  
**Location:** REM/3A14/3C18  
**Art Unit:** 1642  
**Friday, February 18, 2005**

**Case Serial Number:** 09/477082

**From:** Deirdre Arnold  
**Location:** Biotech-Chem Library  
**REM 1A64**  
**Phone:** 571-272-2532

**Deirdre.Arnold@uspto.gov**

### Search Notes

#### RUSH + Score/Length

*Please feel free to contact me if you have any questions or would like to amend the search.*

Thank you for using STIC services.

Regards,  
Deirdre Arnold

**From:** Chan, Christina  
**Sent:** Tuesday, February 08, 2005 12:20 PM  
**To:** Holleran, Anne; STIC-Biotech/ChemLib  
**Subject:** RE: RUSH search for09/477,082

Please rush. Thanks Chris

*Chris Chan*

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

-----Original Message-----

**From:** Holleran, Anne  
**Sent:** Tuesday, February 08, 2005 11:58 AM  
**To:** Chan, Christina  
**Subject:** RUSH search for09/477,082

Please approve and forward to STIC the following RUSH sequence search request. This is for an after-final amendment. Thanks.

Please search the following for 09/477,082:

interference database search for:      SEQ ID NO: 1(na) \*  
SEQ ID NO: 2(na) \*  
SEQ ID NOS: 29-34 (primers) \*\*

SEQ ID NO: 1 and SEQ ID NO: 2 are regions from the 5' untranslated region of a CASP8 gene, and need to be kept together.

\*for SEQ ID NO: 1 and SEQ ID NO: 2, please search standard method and also an oligomer search with hit size limit of 50 nucleotides.

\*\* please perform a score/length sequence search for the primer sequences with a minimum hit length of 15 and a maximum hit length of 40, and a score over length value of 90% or greater.

Thank you.

Anne Holleran  
AU: 1642  
Tel: (571) 272-0833  
RM: Remsen, 3A14

mailbox: Remsen, 3C18

\*\*\*\*\*

STAFF USE ONLY

Searcher: Arnold  
Searcher Phone: 2-2532 9  
Date Searcher Picked up: 2/1/05  
Date Completed: 2/18/05  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA Sequence: # 36  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 75%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

09/477,082

STD 1,2

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case .***